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Sequence alignment A
SEQ ID NO:1
     AAY72630 standard; protein; 317 AA.
     AAY72630;
AC
YY
     15-JUN-2007 (revised)
DT
     02-MAY-2001 (first entry)
XX
     Human follistatin-1 protein.
DE
KW
     Human; follistatin; cytostatic; vulnerary; arthritis; immunomodulatory;
KW
     therapy; liver cirrhosis; Gaucher's disease; vaccine; gene therapy;
KW
     reproductive system disorder; cell growth disorder; Digeorge syndrome;
KW
     tumour; inflammatory bowel disease; anaemia; autoimmune disorder; AIDS;
KW
     Acquired Immune Deficiency Syndrome; SLE; systemic lupus erythematosus;
KW
     Wiskott-Aldrich disorder; cardiovascular disorder; cancer; ischaemia;
KW
     Kaposi sarcoma; hyperproliferative disorder; fibrotic disorder; wound;
KW
     neurodegenerative disorder; congestive heart failure; Crohn's disease;
     Alzheimer's disease; Parkinson's disease; pulmonary fibrosis; BOND_PC;
KW
KW
     follistatin isoform FST317; follistatin isoform FST317 precursor;
KW
     follistatin isoform FST317 precursor [Homo sapiens]; FST; FS;
KW
     follistatin precursor; follistatin; follistatin, isoform CRA_a;
KW
     follistatin, isoform CRA_a [Homo sapiens]; GO122; GO5515; GO5576; GO7276;
     G07389; G08585; G017106; G030509; G042475; G045596; G046882; G07275.
KW
XX
0.9
XX
     W0200105998-A1.
     25-JAN-2001.
     14-JUL-2000; 2000W0-US019198.
XX
     16-JUL-1999; 99US-0144088P.
XX
PA
     (HUMA-) HUMAN GENOME SCI INC.
     Duan RD, Ruben SM;
XX
DR
     WPI; 2001-103150/11.
     PC:NCBI; q15453652.
     PC:SWISSPROT; P19883.
DR
XX
     Nucleic acids encoding follistatin-3, useful for the prevention,
     diagnosis and treatment of e.g. arthritis, liver cirrhosis and Gaucher's
     disease.
PS
     Disclosure; Page 232-233; 245pp; English.
XX
     The present sequence is human follistatin-1 protein, a member of inhibin-
     related proteins. Follistatin-1 protein is 43.2% identical to follistatin
     -3 protein and is an important factor in the regulation of follicle
     development and spermatogenesis in reproductive systems. It also acts as
     an antagonist of activin by preventing the interaction of activin with
     its receptor. In a similar manner follistatin-1 also targets TGF-beta
     superfamily members. Follistatin-3 sequences are used in the prevention.
     diagnosis and treatment of diseases associated with inappropriate
     expression of follistatin-3. The follistatin-3 sequences and their
     agonists or antagonists are useful in the diagnosis, prevention and
     treatment of reproductive system-related disorders; cell growth and
CC
     differentiation disorders (tumours, arthritis, inflammatory bowel
     disease); immune disorders (Digeorge syndrome, anaemia and Wiskott-
     Aldrich disorder); autoimmune disorders (AIDS, Crohn's disease, systemic
     lupus erythematosus-SLE); hyperproliferative disorders (purpura,
     Gaucher's disease, Sezary syndrome); cardiovascular disorders
     (pericarditis, conqestive heart failure, ischaemia); cancers (Kaposi
     sarcoma, lymphoma); neurodegenerative disorders (Alzheimer's disease,
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CC CC CC CC CC CC CC XX	Parkinson's disease); to stimulate wound healing and treat other fibrotic disorders (liver cirrhosis and pulmonary fibrosis) and inhibit angiogenesis. Pollistating DNA sequence is also useful in chromosome identification and in gene therapy Revised record issued on 15-JUN-2007: Enhanced with precomputed information from BOND. Sequence 317 AA;
Ве	ery Match 100.0%; Score 1788; DB 4; Length 317; st Local Similarity 100.0%; Pred. No. 1.4e-118; tothes 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MVRARHQPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQVLYKTELSKEECCSTGR 60
Db	1 mvrarhqpgglcllllllcqfmedrsaqagncwlrqakngrcqvlyktelskeeccstgr 60
Qу	61 LSTSWTEEDVNDNTLFKWMIFNGGAPNCIPCKETCENVDCGPGKKCRMNKKNKPRCVCAP 120
Db	61 LSTSWTEEDVNDNTLFKWMIFNGGAPNCIPCKETCENVDCGPGKKCRMNKKNKPCVCAP 120
Qу	121 DCSNITWKGPVCGLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGSSTCV 180
Db	121 DCSNITWKGPVGGLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGSSTCV 180
Qу	181 VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYSSACHLRKATCLLGRSIGLAYEGKCI 240
Db	181 VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYSSACHLRKATCLLGRSIGLAYEGKCI 240
Qу	241 KAKSCEDIQCTGGKKCLWDFKVGRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEA 300
Db	241 KAKSCEDIQCTGGKKCLWDFKVGRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEA 300
Qу	301 ACSSGVLLEVKHSGSCN 317
Db	301 ACSSGVLLEVKHSGSCN 317